GENETIC EVIDENCE FOR THE EXISTENCE OF TWO SEPARATE POPULATIONS OF *RATTUS FUSCIPES GREYII* ON PEARSON ISLAND, SOUTH AUSTRALIA

by L. H. SCHMITT*

Summary

SCHMITT, L. H. (1975).—Genetic evidence for the existence of two separate populations of *Rattus fuscipes greyii* on Pearson Island, South Australia. *Trans. R. Soc. S. Aust.* **99**(1), 35–38, 28 February 1975.

A study of genetic variation of the enzyme glutamate oxaloacetate transaminase (GOT) reveals the presence of two distinct populations of the southern bush-rat (*Rattus fuscipes greyii*) on Pearson Island. Two allelic genes, *Got-1*^{a} and *Got-1*^{b} are present in the animals collected from the middle and southern sections of the island, while *Got-1*^{a} is absent in animals taken on the northern section. This is discussed in relation to the Pearson Island wallaby which was, until recently, restricted to the northern section of the island.

Introduction

Pearson Island, which lies 60 km off South Australia's west coast, is divided into three discrete sections (Fig. 1). The southern and middle sections are linked by a causeway, while the middle and northern sections are separated by a narrow sea channel. The total area of the island is approximately 325 hectares. The Pearson I. wallaby, *Petrogale* sp. (see Thomas & Delroy 1971, for a discussion on its taxonomic status) and the native rat, *Rattus fuscipes greyii*, are the only terrestrial mammals which are known to inhabit the island.

The native rat, which is found on all three sections of Pearson I., was first described by Thomas (1923) who named it *Rattus murrayi*. Iredale & Troughton (1934) reclassified it as *Rattus greyii murrayi* recognizing its close relationship to *Rattus greyii greyii*, the native bush-rat of mainland South Australia. It was later included in the species *Rattus fuscipes* by Ellerman (1949) as a distinct sub-species, *R. fuscipes murrayi*, along with the mainland form *R.f. greyii*. Recently, Taylor & Horner (1973a) have considered it to be subspecifically indistinguishable from *R.f. greyii*.

Until 1960, the Pearson I. wallaby was only found on the northern section of the island. No evidence could be found to suggest the species ever inhabited the other two sections, despite the suitable habitat available there. The channel appeared to act as a very effective barrier to

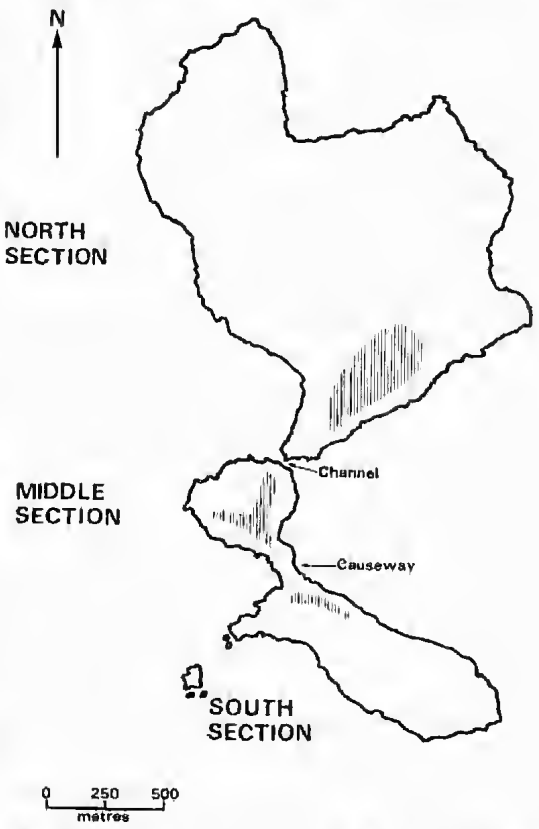

Fig. 1. Map of Pearson Island. Areas where animals were captured are indicated by shading.

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migration between the northern and middle sections. In 1960, six wallabies, including either four or five females, were accidentally released on the middle section and the species is now abundant on the middle and southern sections (Thomas & Delroy 1969).

This paper describes a genetic difference in the *R.f. greyii* population of Pearson I., apparently caused by a restriction in migration across the channel separating the northern and middle sections.

Methods

Specimens of *R.f. greyii* were caught in "Sherman" traps and transported alive to Adelaide. Tissue homogenates were prepared and subjected to starch gel electrophoresis. The electrophoretic buffers (pH 8.0) were essentially the same as those described by Selander *et al.* (1971). The methods used to detect glutamate oxaloacetate transaminase (GOT) activity and determine the subcellular locality of the isozymes were modified from those given by De Lorenzo & Ruddle (1970). Heart extracts were used predominantly, except in the latter procedure when liver extracts were used.

Results and Discussion

Animals were caught from the areas shown in Fig. 1. Seventy-five animals were caught in 218 trap nights, yielding a capture rate of 34%. This is considerably higher than the 2.8% return obtained by Taylor & Horner (1973b) for *R.f. greyii* on the mainland of Australia and Kangaroo I.

Two main regions of GOT activity were present in gels, one migrating cathodally, the other anodally. The cathodal area of activity consisted of a single invariant band. This isozyme predominated in mitochondrial extracts. The anodally migrating isozyme was found in the supernatant fraction and was variable. Three distinct phenotypes, GOT–1A, GOT–1B and GOT–1AB were observed. This variation is consistent with the active enzyme being a dimeric molecule and is similar to that found in man (Chen & Giblett 1971) and the North American old-field mouse, *Peromyscus polionotus* (Selander *et al.* 1971). Genotypes can be assigned to each phenotype, presuming that the difference is under the control of an autosomal locus, with two co-dominant alleles. This locus has been designated *Got-1* and the alleles *Got–1*^{a} and *Got–1*^{b}.

Laboratory matings of *R.f. greyii* individuals from different areas of South Australia, including Pearson I., have been successful. Family data on the inheritance of the GOT variation (Table 1) is cosistent with a 1 locus, 2 allele mode of inheritance.

TABLE 1

Family data on GOT variation

GOT phenotype of parents	Number of matings	Number and GOT phenotype of offspring		
		A	AB	B
A x A	2	3	0	0
A x A*	10	44	0	0
A x B	3	0	9	0
A x AB	1	2	0	0
B x AB	1	0	4	6

* One parent was not scored for GOT phenotype. However, in each of the ten matings it was known to have come from a population apparently monomorphic for the *Got-1*^{a} allele.

The *R.f. greyii* population on the northern section is monomorphic for the *Got 1*^{b} allele, while both *Got–1*^{a} and *Got–1*^{b} are present in the population on the southern and middle sections (Table 2). The genotypic frequencies in the latter population fit the Hardy-Weinberg equilibrium frequencies ($P>0.05$). If the *Got–1*^{a} allele is present in the population on the northern section, then there is a 95% probability that its frequency is less than 3%. In any case, the frequency of the *Got–1*^{b} allele in the northern section is significantly different from its value in the middle and southern sections ($P<<0.001$).

TABLE 2

GOT phenotype distribution in animals caught on Pearson I.

Area caught	Number and GOT phenotype A	AB	B	Frequency of Got-1b
Northern section	0	0	49	1.00
Middle and southern section	10	10	4	0.375

It seems unlikely that the marked difference in allelic frequencies is maintained by selection. All three sections of the island appear to provide very similar habitats for *R.f. greyii*. The observed absence of *Got–1*^{a} from the northern section indicates a severe restriction in gene flow between the areas sampled on the middle and northern sections. The most obvious point of demarcation is the channel separating the two sections. This surprisingly low level of migration between the northern and middle sections is similar to that found in the Pearson I. wallaby.

It would appear improbable that the rats are not physically capable of crossing the channel. When the sea is calm and the tide low, it is

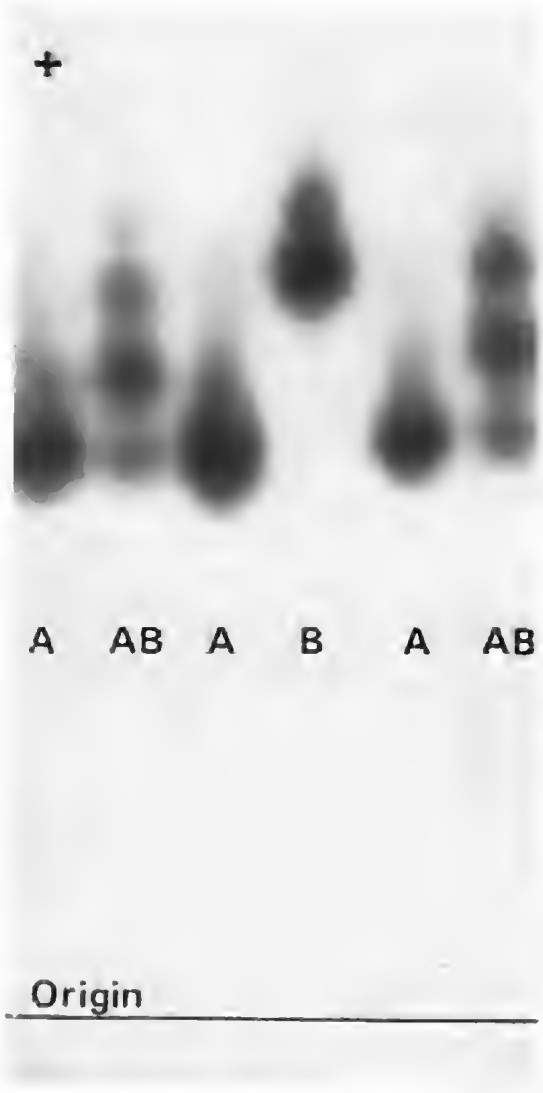

Fig. 2. GOT variation found in *R.f. greyii* from Pearson I. The pattern of variation is in agreement with a dimeric molecule being the active enzyme.

easy for a man to wade or step from rock to rock between the two sections. However, the conformation of the channel is probably in a state of continual change. The relationship between sea level changes and the occurrence of one or more species of small macropod marsupials on small islands off the Western Australian coast has been discussed by Main (1961). From Main's data it appears that Pearson I. has been isolated from the mainland for at least 10,500 years. The northern and middle sections would have remained connected for a considerable time after the isolation of the island. There is some evidence to suggest that since the isolation of Pearson Island from the mainland, the mean sea level on two or more occasions has been about 6 metres above its present level (Twidale, pers. comm.). During these times of high mean sea level, the channel would have been considerably larger than at present.

Thomas & Delroy (1971) suggested that the wallaby did not cross the channel because it found the sea water distasteful. Another possibility is that, because of the action of the sea, there may be strong selective pressures against small animals which wander too close to the edge of the water. Under such an hypothesis, genotypes would be favoured which predisposed animals to an aversion to moving close to the water's edge. This would discourage the animal from crossing between the middle and northern sections.

Various suggestions may be offered to account for the present distribution of the two alleles at the *Got–1* locus. All other populations of *R.f. greyii* studied (Greenly I., Hopkins I., Kangaroo I., Eyre Peninsula and Mount Lofty Ranges) have been found to be monomorphic for the $Got\text{–}1^a$ allele (Schmitt, unpublished). The polymorphism on Pearson I. may have been present before the channel was formed and at that time, or some time afterwards, the $Got\text{–}1^a$ allele was lost from the northern section. Alternatively, one of the alleles could have arisen by mutation, since the channel was formed. If the $Got\text{–}1^b$ allele is the more recent mutant, then it has to be postulated that it subsequently migrated across the channel.

The channel separating the northern and middle sections has not only acted as an effective barrier to migration for the Pearson I. wallaby, but from the genetic evidence presented here, has also had a similar effect on *R.f. greyii*.

Thirteen other gene loci, for which about 70 specimens of *R.f. greyii* from Pearson I. have been scored, are monomorphic on Pearson Island and show no differences across the channel. However, all Pearson I. animals have haemoglobin and malate dehydrogenase proteins that are electrophoretically distinct from all other populations studied (Schmitt, unpublished).

Further studies on the situation described here would be a useful part of any future expeditions to Pearson I.

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